

## SEQUENCE LISTING

&lt;110&gt; SmithKline Beecham Biologicals SA

&lt;120&gt; Novel Compounds

&lt;130&gt; BM45398

&lt;160&gt; 8

&lt;170&gt; FastSEQ for Windows Version 3.0

&lt;210&gt; 1

&lt;211&gt; 615

&lt;212&gt; DNA

<213> *Moraxella catarrhalis*

&lt;400&gt; 1

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gcaatctcgc	tactggacat	gggtaagctt	gatcaagcca	aacagcagtt	ggatgctgct	180
ttatcggctg	atcggcagtt	tgacactgcc	tatcgcacct	tggtcaaagg	ttatcaagct	240
tcggaggatg	ccactcacca	aaccaaagct	caacgcttgt	ttgaaaaggc	gattgaacta	300
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ttgtcaggtg	cgttgattta	ttttgataaa	cctagccgag	ccatcggtta	tgaagggcgt	420
gtggtagcca	tcgaaaatat	ggcatatatt	tattatcatc	aatatgaagc	tgccaaatca	480
ccaacaaaag	atgactataa	taacgccaaa	tcagcacttg	agcgtgcgtt	aatttcaggc	540
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agtgattata	aatag					615

&lt;210&gt; 2

&lt;211&gt; 204

&lt;212&gt; PRT

<213> *Moraxella catarrhalis*

&lt;400&gt; 2

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Leu	Ala	Gln	Ile	Arg	Thr	Gln	Ile	Ala	Ile	Ser	Leu	Leu	Asp	Met	Gly
		35				40					45				
Lys	Leu	Asp	Gln	Ala	Lys	Gln	Gln	Leu	Asp	Ala	Ala	Leu	Ser	Ala	Asp
	50				55				60						
Arg	Gln	Phe	Ala	Pro	Ala	Tyr	Arg	Thr	Leu	Ala	Lys	Val	Tyr	Gln	Ala
65					70				75					80	
Ser	Glu	Asp	Ala	Thr	His	Gln	Thr	Lys	Ala	Gln	Arg	Leu	Phe	Glu	Lys
			85					90					95		
Ala	Ile	Glu	Leu	Asn	Pro	Lys	Asp	Met	Gln	Ser	Tyr	Met	Asp	Tyr	Gly
		100					105					110			
Phe	Tyr	Leu	Val	Gln	Met	Gly	Asp	Leu	Ser	Gly	Ala	Leu	Ile	Tyr	Phe
	115					120					125				
Asp	Lys	Pro	Ser	Arg	Ala	Ile	Gly	Tyr	Glu	Gly	Arg	Val	Val	Ala	Ile
	130				135				140						
Glu	Asn	Met	Ala	Tyr	Ile	Tyr	Tyr	His	Gln	Tyr	Glu	Ala	Ala	Lys	Ser
145					150				155					160	
Pro	Thr	Lys	Asp	Asp	Tyr	Asn	Asn	Ala	Lys	Ser	Ala	Leu	Glu	Arg	Ala

10/069544

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 180 185 190  
 Leu Leu Ser Asp Tyr Lys Leu L u Ser Asp Tyr Lys  
 195 200

<210> 3  
 <211> 612  
 <212> DNA  
 <213> *Moraxella catarrhalis*

<400> 3  
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 ttatcggtcg atcggcagtt tgcacctgcc tatcgcacct tggcaaagggt ttatcaagct 240  
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 aatcctaaag atatgcaaag ttatatggat tatggatttt atttgggtgca gatgggggac 360  
 ttgtcagggtg cggttgattta ttttgataaa cctagccgag ccatcggtta tgaagggcgt 420  
 gtggtagcca tcgaaaatat ggcatatatt tattatcatc aatatgaagc tgccaaatca 480  
 ccaacaaaag atgactataa taacgcaaaa tcagcacttg agcgtgcgtt aatttcaggc 540  
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<210> 4  
 <211> 204  
 <212> PRT  
 <213> *Moraxella catarrhalis*

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 Leu Ala Gln Ile Arg Thr Gln Ile Ala Ile Ser Leu Leu Asp Met Gly  
 35 40 45  
 Lys Leu Asp Gln Ala Lys Gln Leu Asp Ala Ala Leu Ser Ala Asp  
 50 55 60  
 Arg Gln Phe Ala Pro Ala Tyr Arg Thr Leu Ala Lys Val Tyr Gln Ala  
 65 70 75 80  
 Ser Glu Asp Ala Thr His Gln Thr Lys Ala Gln Arg Leu Phe Glu Lys  
 85 90 95  
 Ala Ile Glu Leu Asn Pro Lys Asp Met Gln Ser Tyr Met Asp Tyr Gly  
 100 105 110  
 Phe Tyr Leu Val Gln Met Gly Asp Leu Ser Gly Ala Leu Ile Tyr Phe  
 115 120 125  
 Asp Lys Pro Ser Arg Ala Ile Gly Tyr Glu Gly Arg Val Val Ala Ile  
 130 135 140  
 Glu Asn Met Ala Tyr Ile Tyr Tyr His Gln Tyr Glu Ala Ala Lys Ser  
 145 150 155 160  
 Pro Thr Lys Asp Asp Tyr Asn Asn Ala Lys Ser Ala Leu Glu Arg Ala  
 165 170 175  
 Leu Ile Ser Gly Thr Gln His Asp Glu Ile Lys Lys Ser Tyr Asp Lys  
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 Leu Leu Ser Asp Tyr Lys Leu Leu Ser Asp Tyr Lys  
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WO 01/09330

PCT/EP00/07281

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<213> Artificial Sequence

<220>  
<223> primer

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<210> 6  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 6  
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<210> 7  
<211> 38  
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<220>  
<223> primer

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<210> 8  
<211> 60  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

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## SEQUENCE LISTING

<110> Joelle Thonnard

<120> Novel Compounds

<130> BM45398

<150> 99180040.8

<151> 1999-07-30

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 615

<212> DNA

<213> *Moraxella catarrhalis*

<400> 1

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aacccaaatt     120
gcaatctcgc tactggacat gggtaagctt gatcaagcca aacagcagtt
ggatgctgct     180
ttatcggctg atcggcagtt tgcacctgcc tatcgcacct tggcaaagggt
ttatcaagct     240
tcggaggatg ccactcacca aaccaaagct caacgcttgt ttgaaaaggc
gattgaacta     300
aatcctaaag atatgcaaag ttatatggat tatggatttt atttggtgca
gatgggggac     360
ttgtcagggtg cgttgattta ttttgataaa cctagccgag ccatcggtta
tgaagggcgt     420
gtggtagcca tcgaaaatat ggcatatatt tattatcatc aatatgaagc
tgccaaatca     480
ccaacaaaag atgactataa taacgccaaa tcagcacttg agcgtgcgtt
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<210> 2  
 <211> 204  
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 <213> Moraxella catarrhalis

<400> 2  
 Met Lys Ile Arg Val Lys Trp Pro Met Val Met Ala Met Gly Leu Val  
 1 5 10 15  
 Leu Ser Ala Cys Gln Ser Thr Pro Ile Pro Pro Lys Asn Asn Pro Gln  
 20 25 30  
 Leu Ala Gln Ile Arg Thr Gln Ile Ala Ile Ser Leu Leu Asp Met Gly  
 35 40 45  
 Lys Leu Asp Gln Ala Lys Gln Gln Leu Asp Ala Ala Leu Ser Ala Asp  
 50 55 60  
 Arg Gln Phe Ala Pro Ala Tyr Arg Thr Leu Ala Lys Val Tyr Gln Ala  
 65 70 75 80  
 Ser Glu Asp Ala Thr His Gln Thr Lys Ala Gln Arg Leu Phe Glu Lys  
 85 90 95  
 Ala Ile Glu Leu Asn Pro Lys Asp Met Gln Ser Tyr Met Asp Tyr Gly  
 100 105 110  
 Phe Tyr Leu Val Gln Met Gly Asp Leu Ser Gly Ala Leu Ile Tyr Phe  
 115 120 125  
 Asp Lys Pro Ser Arg Ala Ile Gly Tyr Glu Gly Arg Val Val Ala Ile  
 130 135 140  
 Glu Asn Met Ala Tyr Ile Tyr Tyr His Gln Tyr Glu Ala Ala Lys Ser  
 145 150 155 160  
 Pro Thr Lys Asp Asp Tyr Asn Asn Ala Lys Ser Ala Leu Glu Arg Ala  
 165 170 175  
 Leu Ile Ser Gly Thr Gln His Asp Glu Ile Lys Lys Ser Tyr Asp Lys  
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 Leu Leu Ser Asp Tyr Lys Leu Leu Ser Asp Tyr Lys  
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<210> 3  
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 aacccaaatt 120

gcaatctcgc tactggacat gggtaagctt gatcaagcca aacagcagtt  
ggatgctgct 180  
ttatcggctg atcggcagtt tgcacctgcc tatcgcacct tggcaaaggt  
ttatcaagct 240  
tcggaggatg ccactcacca aaccaaagct caacgcttgt ttgaaaaggc  
gattgaacta 300  
aatcctaaag atatgcaaag ttatatggat tatggatttt atttggtgca  
gatgggggac 360  
ttgtcagggt cgttgattta ttttgataaa cctagccgag ccatcggtta  
tgaagggcgt 420  
gtggtagcca tcgaaaatat ggcatatatatt tattatcatc aatatgaagc  
tgccaaatca 480  
ccaacaaaag atgactataa taacgccaaa tcagcacttg agcgtgcggt  
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<210> 4  
<211> 204  
<212> PRT  
<213> Moraxella catarrhalis

<400> 4  
Met Lys Ile Arg Val Lys Trp Pro Met Val Met Ala Met Gly Leu Val  
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Leu Ser Ala Cys Gln Ser Thr Pro Ile Pro Pro Lys Asn Asn Pro Gln  
20 25 30  
Leu Ala Gln Ile Arg Thr Gln Ile Ala Ile Ser Leu Leu Asp Met Gly  
35 40 45  
Lys Leu Asp Gln Ala Lys Gln Gln Leu Asp Ala Ala Leu Ser Ala Asp  
50 55 60  
Arg Gln Phe Ala Pro Ala Tyr Arg Thr Leu Ala Lys Val Tyr Gln Ala  
65 70 75 80  
Ser Glu Asp Ala Thr His Gln Thr Lys Ala Gln Arg Leu Phe Glu Lys  
85 90 95  
Ala Ile Glu Leu Asn Pro Lys Asp Met Gln Ser Tyr Met Asp Tyr Gly  
100 105 110  
Phe Tyr Leu Val Gln Met Gly Asp Leu Ser Gly Ala Leu Ile Tyr Phe  
115 120 125  
Asp Lys Pro Ser Arg Ala Ile Gly Tyr Glu Gly Arg Val Val Ala Ile  
130 135 140  
Glu Asn Met Ala Tyr Ile Tyr Tyr His Gln Tyr Glu Ala Ala Lys Ser  
145 150 155 160

Pro	Thr	Lys	Asp	Asp	Tyr	Asn	Asn	Ala	Lys	Ser	Ala	Leu	Glu	Arg	Ala
				165					170					175	
Leu	Ile	Ser	Gly	Thr	Gln	His	Asp	Glu	Ile	Lys	Lys	Ser	Tyr	Asp	Lys
			180					185					190		
Leu	Leu	Ser	Asp	Tyr	Lys	Leu	Leu	Ser	Asp	Tyr	Lys				
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<210> 6  
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 <213> Artificial Sequence

<220>  
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<400> 6  
 ggctgaaaat cttctctcat cc  
 22

<210> 7  
 <211> 38  
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 <223> primer

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 38

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